

45 (New). A method for producing a transgenic plant, comprising transforming a plant cell with the nucleic acid molecule of claim 29 or 30 operatively associated with a regulatory sequence containing transcriptional and translational regulatory elements that control expression of the nucleic acid in the plant cell.

46 (New). A genetically-engineered plant in which an endogenous *SCARECROW* gene comprising a nucleic acid sequence that encodes a polypeptide comprising the amino acid sequence of SEQ ID NO: 96 is disrupted or inactivated so that cell division is decreased in roots, resulting in thinner root development.--

REMARKS

The specification has been amended to correct the identification of the sequences disclosed therein by their respective SEQ ID NOs as found in the Substitute Sequence Listing being submitted concurrently herewith. Two inadvertent typographical errors have been corrected so that the specification agrees with the titles on FIGS. 25A-B and FIG. 29A. Applicants have also corrected the spelling of the word 'sequence' in the description of FIGS. 25A-B. No new matter is introduced by virtue of these amendments.

Claims 29-46 will be pending and under consideration upon entry of this amendment. Claims 1-10, 17-22, 27 and 28, corresponding to Group I, have been canceled and replaced by new claims 29-62. Claims 11-16 and 23-26 have been canceled without prejudice as drawn to non-elected inventions, in view of the restriction requirement. Applicants reserve the right to prosecute the non-elected subject matter in one or more related applications. New claims 29-46 are supported by the specification and by the original claims as filed. Specific support for each of new claims 29-46 may be found in the following Table of Claim Support:

TABLE OF CLAIM SUPPORT

New Claim No.	Corresponding Old Claim No.	Support in Specification
29	--	page 26, line 32 - page 27, line 1 page 32, lines 10-13 Figures 25A-B
30	2	page 26, line 32 - page 27, line 7 Figures 25A-B
31	7	page 33, lines 6-9
32	8	page 33, lines 6-16
33	9	page 33, lines 6-16 page 43, line 29 - page 44, line 2
34	10	page 33, lines 6-16 page 43, line 29 - page 44, line 2
35	--	page 24, lines 21-29 page 59, line 15 - page 65, line 34
36	17	page 26, lines 1-16 page 62, line 21 - page 65, line 33 page 67, lines 2-19
37	18	page 26, lines 1-10 page 63, line 20 - page 64, line 16 page 66, line 35 - page 68, line 4

New Claim No.	Corresponding Old Claim No.	Support in Specification
38	27	page 26, lines 1-16 page 67, lines 21-27
39	28	page 26, lines 1-10 page 67, lines 21-27
40	19	page 24, lines 21-29 page 59, line 15 - page 65, line 34
41	20	page 62, lines 21-28
42	21	page 26, lines 1-16 page 64, lines 20-25
43	--	page 26, lines 1-16 page 64, lines 20-29
44	--	page 33, lines 6-16 page 43, line 29 - page 44, line 2
45	--	page 33, lines 6-16 page 59, lines 15-27 page 62, lines 21-28
46	22	page 26, lines 1-16 page 59, lines 15-27 page 64, lines 20-32

No new matter is added by way of the amendments to the specification or claims. Applicants respectfully request the entry of the Sequence Listing, submitted herewith, and the foregoing amendments and remarks into the file of the instant application.

THE RESTRICTION REQUIREMENT

The Examiner has required an election under 35 U.S.C. § 121 of one of the following inventions:

- Group I: Claims 1-10, 17-22, 27 and 28, drawn to polynucleotides encoding scarecrow proteins, and vectors, host cells and transgenic plants comprising same, classified in class 536, subclass 23.6.
- Group II: Claims 11-14, drawn to scarecrow proteins, classified in class 530, subclass 350.
- Group III: Claims 15 and 16, drawn to antibodies, classified in class 530, subclass 387.1.
- Group IV: Claims 23-26, drawn to transgenic plants comprising a scarecrow promoter, classified in class 800, subclass 295.

The Examiner contends that the inventions of the above Groups are distinct, each from the other.

Further, the Examiner has required an election of a single disclosed species (*i.e.*, one polynucleotide by SEQ ID NO: and one polypeptide which it encodes by SEQ ID NO:) within each group for prosecution on the merits, to which the claims shall be restricted if no generic claim is held to be allowable.

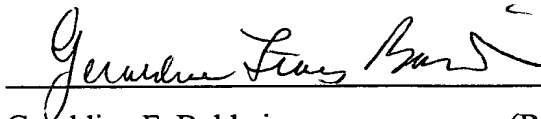
In order to be fully responsive, Applicants hereby elect the invention of Group I, claims 1-10, 17-22, 27 and 28, drawn to polynucleotides encoding scarecrow proteins, and vectors, host cells and transgenic plants comprising same, classified in class 536, subclass 23.6. Further, Applicants provisionally elect with traverse the following species: the *Zea mays* scarecrow (ZCR) nucleic acid sequence (SEQ ID NO: 95). Claims readable on the elected species within elected Group I are new claims 29-46.

Submitted herewith is a Supplemental Information Disclosure Statement and a List of References Cited listing references BW-BZ and CA-CF, together with a copy of each of references BW, CA, CB, CD and CF. On July 8, 1999, an Information Disclosure Statement was submitted listing references AA-BV. It is requested that all the listed references be reviewed and made of record in the file of this application.

Applicants respectfully request that the above-made amendments and remarks be entered and made of record in the file history of the application.

Respectfully submitted,

Date: September 12, 2001

 31,232

Geraldine F. Baldwin

(Reg. No.)

PENNIE & EDMONDS LLP

1155 Avenue of the Americas

New York, New York 10036-2711

(212) 790-9090

Enclosures:

Exhibit A: Marked Up Version of Replacement Paragraphs of the Specification

Exhibit B: Claims Pending After Entry of the Amendment dated September 12, 2001

EXHIBIT A

Marked Up Version of Replacement Paragraphs of the Specification U.S. Patent Application Serial No. 09/265,585

Matter that has been deleted from the paragraphs is indicated by brackets and matter that has been added to the paragraphs is indicated by double underlining. Matter that was originally underlined in the specification remains singly underlined to distinguish it from matter that has been added.

On page 17, line 15, please amend the paragraph beginning "FIG. 11B." as follows:

FIG. 11B. Partial nucleotide sequence (SEQ ID NO:[25] 26) and deduced amino acid sequence (SEQ ID NO:[26] 27) of the maize *SCLm1* gene (Zm-Sc12).

On page 18, line 4, please amend the paragraph beginning "15A-S." as follows:

FIGS. 15A-S. Comparison of the partial and complete amino acid sequences of several plant members of the *SCARECROW* family of genes. The amino acid sequences are aligned in a manner that maximizes amino acid sequence similarity and identity among *SCR* family members. Each sequence shown is continuous except where noted otherwise; the dots are inserted between two sequence segments in order to align homologous segments. "X" in the middle of a sequence indicates ambiguity in the corresponding nucleotide sequence and, possible termination of the ORF at the "X" residue site. "X" at the end of a sequence indicates termination of the ORF at the "X" residue site. The numbering of the amino acid residues is shown at the bottom of each figure and is based on the Arabidopsis *SCR* amino acid sequence. Conserved Motifs I through VI are indicated by the various dashed lines above the figures. The new and old names of the family members are shown in FIG. 15A. The sequences of *SCR*, Tf1 and Tf4 are of the complete *SCR* protein. The sequence identifier numbers are as follows: SCR (SEQ ID NO: 2); 3989 (SEQ ID NO: 36); 12398 (SEQ ID NO: 52); 4871 (SEQ ID NO: 46); 11846 (SEQ ID NO: 59); 2504 (SEQ ID NO: 44); 3935 (SEQ ID NO: 21); 11261 (SEQ ID NO: 50); 713 (SEQ ID NO: 43); 10964 (SEQ ID NO: 48); 23196 (SEQ ID NO: 58); Tf1 (SEQ ID NO: 34); Tf4 (SEQ ID NO: 35); 18310 (SEQ ID NO: 37); 18652 (SEQ ID NO: 54); 4818 (SEQ ID NO: 19); 21729

(SEQ ID NO: 151); 1110 (SEQ ID NO: 23); 174 (SEQ ID NO: 42); and 33/08 (SEQ ID NO: 41)[See Table 1 for the identity and the sequence identifier number of each sequence shown in these figures].

On page 22, line 3, please amend the paragraph beginning "FIG. 25." as follows:

[FIG. 25] FIG25A-B. Maize Scarecrow gene. The nucleotide (SEQ ID NO: 95) and deduced amino acid [sequence] sequence (SEQ ID NO: 96) of the maize scarecrow gene (*ZCR*) is shown. The amino acid numbers are shown on the right, while the nucleotides are numbered on the left.

On page 22, line 7, please amend the paragraph beginning "FIG. 26." as follows:

[FIG. 26] FIG. 26A. Amino acid sequence alignment of maize *ZCR* (SEQ ID NO: 96) and Arabidopsis *SCR* (SEQ ID NO: 2). Identical residues are marked by asterisks. In addition, three copies of an LXXLL motif are underlined.

On page 22, line 27, please amend the paragraph beginning "FIG. 28A-AH." as follows:

FIGS. 28A-AH. The partial nucleotide and amino acid sequences of Arabidopsis EST's that encode members of the SCARECROW-like (*SCL*) gene family (SEQ ID NOS: 68-94, 23, 21, 19, 46, 50, 54, and 58 respectively). "N" indicates an unknown base. [See Table 2 for the identity and the sequence identifier number of each sequence shown in these figures.]

On page 22, line 33 to page 23, line 8, please amend the paragraph beginning "FIG. 29." as follows:

FIG. 29. Alignment of the Arabidopsis GRAS gene products (SCL3 (SEQ ID NO: 21), SCL11 (SEQ ID NO: 50), SCL9 (SEQ ID NO: 113), SCL14 (SEQ ID NO: 58), SCL16 (SEQ ID NO: 126), SCL13 (SEQ ID NO: 54), SCL5 (SEQ ID NO: 128), SCL1 (SEQ ID NO: 23), SCL8 (SEQ ID NO: 116), SCL4 (SEQ ID NO: 117), SCL7 (SEQ ID NO: 52), SCL6 (SEQ ID NO: 46; residues 21-378), SCL15 (SEQ ID NO: 119), SCL18 (SEQ ID NO: 120), GAI (SEQ ID NO: 150), RGA (SEQ ID NO: 149), RGAL (SEQ ID NO: 123), SCL 19 (SEQ ID NO: 130 and SCR (SEQ

ID NO: 2). The highly conserved region of the GRAS products can be divided into five recognizable motifs, indicated in the figure. See also, for example, Section 5.1.5., *infra*. The absolutely conserved residues within the VHIID (SEQ ID NO: 145) and SAW (SEQ ID NO: 146) motifs are highlighted in bold, as are the hydrophobic residues of the leucine heptads, the P-F-Y-R-E residues of the PFYRE motif (SEQ ID NO: 147), and the two short sequences that define the end of the VHIID motif (SEQ ID NO: 145) and the beginning of the PFYRE motif (SEQ ID NO: 147). The @ symbol in the alignment indicates the location of an apparent insertion in the SCL3 gene (SEQ ID NO: 148). The deduced amino acid sequence of the insertion is shown at the bottom of the figure.

On page 24, line 1, please amend the paragraph beginning "FIG. 33." as follows:

FIG. 33. CBPBTT44 Partial cDNA (SEQ ID NO: 104) and Amino Acid Sequence (SEQ ID NO: 105). The partial nucleotide and amino acid sequence of CBPBTT44, a closely related gene to the maize ZCR gene.

On page 24, line 4, please amend the paragraph beginning "FIG. 34." as follows:

FIG. 34. Alignment of the Arabidopsis SCR (SEQ ID NO: 2, positions 364-653), the maize ZCR (SEQ ID NO: 101) and the CBPBTT44 (SEQ ID NO: 102) amino acid sequence. As shown in bold, all three genes contain the leucine heptad repeats. The alignment further shows that all three genes share a high degree of homology.

On page 37, line 10, please amend the section beginning "PRIMERS:" as follows:

PRIMERS:

Forward:

Name: SCR5AII (23-mer, 2 inosines, 64-mix)
A.A. code: HFTANQAI (SEQ ID NO: 134)

DNA Sequence: 5' CAT/C TTT/C ACI GCI AAT/C CAA/G GCN AT 3'
(SEQ ID NO: 133)

Name: SCR5B (29-mer, 1 inosine, 144-mix)

A.A. code: VHIID(L/F)D (SEQ ID NO: 136)

DNA Sequence: 5' ACGTCTCGA GTI CAT/C ATA/C/T ATA/C/T GAT/C
TTN GA 3' (SEQ ID NO: 135)

Name: 1F

A.A. code: LQCAEAV (SEQ ID NO: 138)

DNA Sequence: (T/C)TI CA(A/G) TG(T/C GCI GA(A/G) GCN GT
(SEQ ID NO: 137)

Reverse:

Name: SCR3AII (23-mer, 2 inosines, 128-mix)

A.A. code: PGGPP(H/N/K) (V/L/F)R' (SEQ ID NO: 140)

DNA Sequence: 5' CG/T CCA/C GTG/T TGG IGG ICC NCC NGG 3'
(SEQ ID NO: 139)

Name: 1R

A.A. code: AFQVFNGI (SEQ ID NO: 142)

DNA Sequence: AT ICC (A/G)TT (A/G)AA IAC (C/T)TG (A/G)AA NGC
(SEQ ID NO: 141)

Name: 4R

A.A. code: QWPGLFHI (SEQ ID NO: 144)

DNA Sequence: AT (A/G)TG (A/G)AA IA(A/G) NCC IGG CCA (C/T)TG
(SEQ ID NO: 143)

I = inosine

N = A/C/G/T

Useful primer combinations include the following:

SCR5AII+SCR3AII; SCR5B+SCR3AII; IF+IR; and IF+4R

EXHIBIT B

Claims Pending After Entry of the Amendment dated September 12, 2001

U.S. Patent Application Serial No. 09/265,585

29. An isolated nucleic acid molecule wherein the nucleic acid molecule comprises SEQ ID NO: 95 or the complement thereof.

30. An isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a polypeptide comprising the amino acid sequence of SEQ ID NO: 96.

31. A DNA vector containing the nucleic acid molecule of claim 29 or 30.

32. An expression vector containing the nucleic acid molecule of claim 29 or 30, operatively associated with a regulatory sequence containing transcriptional and translational regulatory elements that control expression of the nucleic acid in a host cell.

33. A genetically-engineered host cell containing the nucleic acid molecule of claim 29 or 30.

34. A genetically-engineered host cell containing the nucleic acid molecule of claim 29 or 30, operatively associated with a regulatory sequence containing transcriptional and translational regulatory elements that control expression of the nucleic acid in a host cell.

35. A genetically-engineered plant containing the nucleic acid molecule of claim 29 or 30.

36. A plant genetically-engineered to overexpress or underexpress a SCARECROW protein or polypeptide, said protein or polypeptide being encoded by the nucleic acid molecule of claim 29 or 30, wherein cell division in the plant is modified, and root and/or stem development is altered.

37. A plant genetically-engineered to overexpress a SCARECROW protein or polypeptide comprising SEQ ID NO: 96, so that cell division is increased in roots.

38. A plant genetically-engineered to overexpress or underexpress a SCARECROW protein or polypeptide comprising SEQ ID NO: 96, wherein the gravitropism of the stem or hypocotyl is altered.

39. The plant of claim 38 that is less susceptible to lodging than a wild-type plant.

40. A transgenic plant containing a transgene comprising the nucleic acid molecule of claim 29 or 30.

41. The transgenic plant of claim 40 wherein the nucleic acid molecule is operatively associated with a regulatory sequence containing transcriptional and translational regulatory elements that control expression of the nucleic acid in a transgenic plant cell.

42. The transgenic plant of claim 40, wherein the transgene encodes an antisense nucleotide sequence that suppresses expression of an endogenous *SCARECROW* protein or polypeptide comprising SEQ ID NO: 96, so that cell division is decreased in roots, resulting in thinner root development.

43. The transgenic plant of claim 40, wherein the transgene encodes a ribozyme complementary to a nucleotide sequence encoding an endogenous *SCARECROW* protein or polypeptide comprising SEQ ID NO: 96, so that cell division is decreased in roots, resulting in thinner root development.

44. A method for expressing a nucleic acid that encodes a SCARECROW protein or polypeptide comprising SEQ ID NO: 96 in a host cell, comprising:

- (a) culturing the genetically-engineered host cell of claim 33 or 34; and
- (b) inducing the transcriptional and translational regulatory elements that control expression of the nucleic acid.

45. A method for producing a transgenic plant, comprising transforming a plant cell with the nucleic acid molecule of claim 29 or 30 operatively associated with a

regulatory sequence containing transcriptional and translational regulatory elements that control expression of the nucleic acid in the plant cell.

46. A genetically-engineered plant in which an endogenous *SCARECROW* gene comprising a nucleic acid sequence that encodes a polypeptide comprising the amino acid sequence of SEQ ID NO: 96 is disrupted or inactivated so that cell division is decreased in roots, resulting in thinner root development.